

Figure 1. The *Naegleria* agent causes the rapid disappearance of thiamin from the growth medium of rat glioma C6 cells.

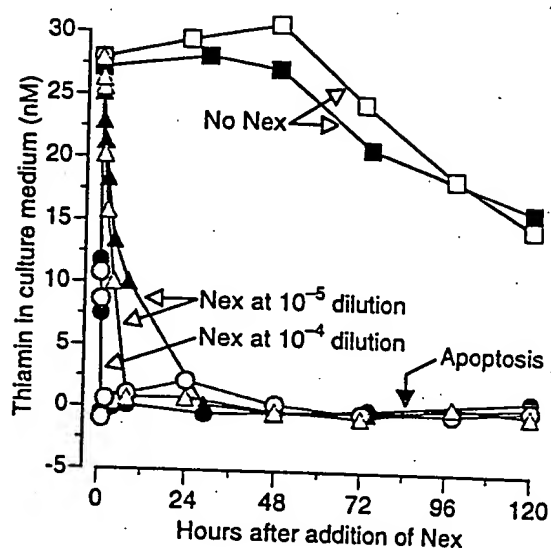


Figure 2. The addition of thiamin can reverse progress of rat glioma C6 cells toward apoptosis induced by the *Naegleria* agent. Thiamin added at 12 hour intervals reversed progress until death of the cells had already occurred on day 4.5.

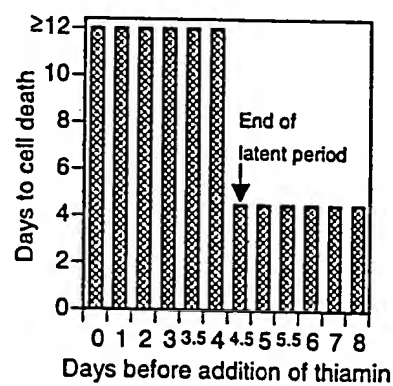
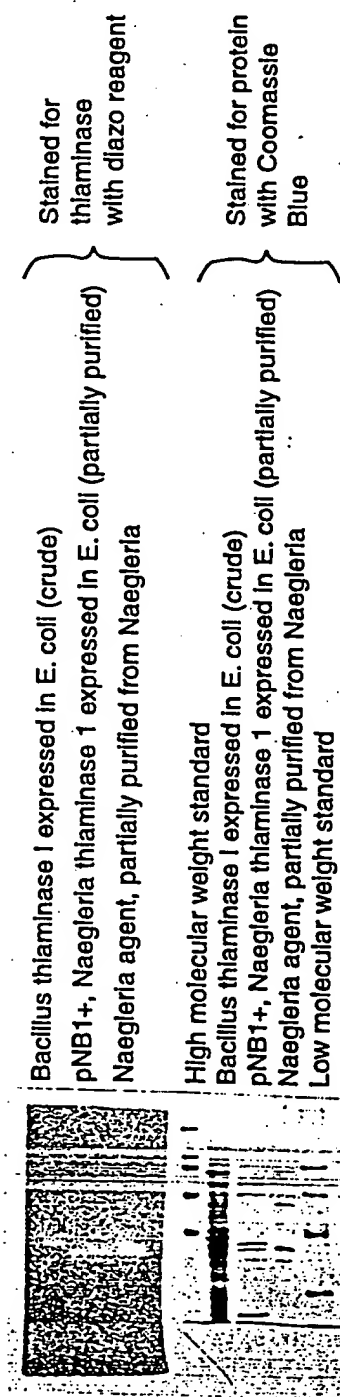


Figure 3. An SDS-polyacrylamide gel stained for thiaminase and for protein. The *Naegleria* agent was purified through preparative isoelectric focusing (see Example 3).



[illegible]

ATGTCACCTCAACCAAGACACTCACTGTTGGTCTCTTCCCATATCTTCTTCTTGGAAATGAAATGGCAACGAAGTTAA
ATTGATCAATTTGATCAAGGATGTTTTTGCCAATCACTAGGTTTCCGGATATAATATCGAATATACCGAATTTGATTGTTACA
GTGATGCTAGTCTTCAAAGTCTTCCAGATGTTTTCTCAACTGATAGCATTTTCTCCATATCTTGTCTTTTGGGTGGT
GTCAAGAGTTTGGATGAATCATTGGTTCGTGGTGTACTGGTGATTGTCATAGTTTTGTTTCTCAAGTGCTCTGTCAA
TGGTTCGGTTTTATGGTTTCCCACAATACTTGTGCTCAAACTTTTTATGTCTCACCAAATGGTACTCAACAAGCATCTT
CCCTTTTAGAATTGGCTCAAAGGTTGGTTATGAACAAATTGTTTTATCCAGATGTTGCCTCTTCTAGTCTTTTCACAGTT
TTCGGATTGTATCAACAATTACTCCAATCATCATCAGCTGCAGTTGATATCAAGGCCCTCTGATCTTCCACAATCTGG
TGACCAAGTCAACAAGGATATCACTCAAAAATATAGAACCATTTTGGATTCAACAGTTGTTGCCTCTCAAAGAGAATATA
TTAACTCTGTAAAGCAAGGTAAACCAATTTCAAACACTATGTCCGATATAGTGAAAGTATGTGTGAAATTAAGGATATC
ATCAGAGATCAACAATACAATGTTCAACTCATTGGTACCTCTGATAAGCCATACGTTTATACTGATGTTTTGGCTTTGAA
TTCCAATTTGTGTGATGAAAAGCAAAAGGTTGCTGTTGAAGTTATCAAGAATTTATTGACTAATACTTTAGTTTTGGACT
TGTGGGTCTCGGATTAACCTCTCCCAGCCAACAAGAATGGTATTGCTCATTGGCTAAATCATCAAACCTTTATGCTCAA
TTGAGCCAACAATTCGATGCCAAGGAAAGTGAAGTTAGAGTTTTGAGATGTGTTGACTTTGCTAACAAGGAAGTTAAGAA
TTGTGCTGGTGTCTTGAGACCATTCTTCAACATATTGCTGTTGCTACTTTGCGTTGTTTGACTGCTGACACTGTCGAAA
AGGCTAAGAGTGGTCACCTGGTATGCCAATTGGTATGTCAACCAATTGCCTATGTTTTGTGGAAGTTCTTCTTCAAATCA
TCTAAGGATGATGCTCAATTGGTTGAACAGAGATAGATTTGTTTTGAGTAATGGTCACGGTTGTACATTGCTTTATGCCAT
GTTGCACCTCACTGATTGTAACTTGTAGTTTGGATGATCTCAAGAATTTCAGAAGTTTGCATTCCAAGACTCCTGGTCACC
CAGAATATGGTCACACTGAAGGTGTTGATGCTACTACTGGTCCATTGGGTCAAGGTGTTTGAATGCTATTGGTATGGCT
CTCTCTGAAGCTCACTTGGCTGCTCGTTTTCAATAAGGATGGACAAAATATCTTTGATCACCACACCTATGTTTTCTTGG
TGATGGTTGTTTGTATGGAACGTGTTGCTATGGAAGGTCTCTCATTGCTGGTCACCAAAAGTTGAACAAGTTGATTGTTT
TCTATGATGACAATAGTATTACTATTGATGGTAAGACTGAATTGACCTTTACTCAAAATCTCCAGAAGTCATGAGAGGT
TTTGGATGGCACGTAATTGTTGTCGACAAGGCTGATAATGACTTGGTTGGTATTAAGGAAGCTATTTTGAAGCTCACAC
TGTTACTGACAAGCCAATCATGATCGTTTGTAAAGACTACAATTGGTTATTCTCAAAAGTTCAAGGTACTGCTAAGGTTT
ACGGTTCTCCATTGGGTGCTGATGGATTGAAGAATTTGAAGGAACTTGTGGTTTCACTGGTAATGATTCTTCCATGTT
CCAGAAATTTGTCAGAAAGGACTTTGCTACTGTCAATTAATAGAAATAGTGAAAAGCTCTCTCAATGGAAGCAAGTTAAATC
TGCCATGATACCACTCATGCTACTGAATCCCAACTCCTCCAAAGAATGATTAATACGAATTGGAAGGTGATGTTATGG
AAAAGTTGCCAAAATACCTCGAACAAAAGAAGATTGCTACCAGATCTACATCTCAACAAGTTTTGAATGCCATCTATCCA
CTCATCTCTTCTCTCGTTGGTGGTTTCACTGACTTGACTCCATCCAACCTTGACTGATGTAAGTGGATGTCAAGATTTCCA
ACCAACAATAGAGTTGGTAGATATATCAGATTTGGTGTCCGTGAACATGCCATGGTTGCTATTGCCAATGGTATTCTCT
ATCATGGTGTCTTAGAACCTATGTTGGTACATTCTTGAACCTTGGCTTCATATGCTTTGGGTGCTATCAGATTGAGTGCC
TTGCTGGTCTTCCAAATATTTATGTTTTCACTCATGACAGTATTGGTCTTGGTCAAGATGGTCCAACCTCAACCACTGT
TGAAGTTTTACCAATGTTGATAGCCATTCCAAATCACATTGTTTTTCAAGCTGCTGATGGTAGAGAAACCAGTGGTGCCT
ATTGTTGGGCTGTTCAATCAAAGAAGACTCCATCCTCAATGATTCTTCTCGTCAAGATTTGCCACAATTGACTGGTACT
GATATTTCAAAGGTTGCTTTTGGGTGCCATGTTATCCAAGGTGATGCTACTCCTGATGTTGTCTTGGTGGTACTGGTTC
TGAAGTTTCCCTCATGTTTGAAGCTGCTGAAAAGTTGAAGGCTAACCTTAAGGTTAACGTTGTTTCCATGCCAAGTTGGG
AATTGTTTGTTCGTCAATCAGAAGAATACAGGAAGACTGTCTTCCAGATGGTATTCCAGTTGTGAGTGCCGAAGCTTCA
TCAACCTTTGGTTGGACAAGCTTTGCTCAGTATGCTGTTGGTATGACTACTTTCGGTGCTAGTGCTGCTGCTGAAGAAGT
TTACAAACTCCTCAAGATTACCTCAGACAATGTTGCTGAAAAGGCCACCAAAATTGGTTACCAAGTATGGTAAGCAAGCTC
CAAGACTCAGCTTGCTCTTGTGGTGAAGAAGCTCTAA

Figure 5. The amino acid sequence encoded by the entire *Naegleria* TTK gene

MSTQPKTLTVGLFPYLPSPWNENGNEVKLINLIKDVLPQVSGYNIEYTEFDCYSDASLQSLPDVFSTDSIFLPYLVS LGG
VKSLDESLVRGVTGDLHSFVSSASVNGSVYGFPOYLCSNFLSSPNGTQQASSLLELAQKVGYEQIVYPDVASSSSFTV
FGLYQQLLQSSSSAAVDIKASDLPQSGDQVNKDITQKYRTILDSTVVASQREYINSVKQGPISNYYVGYSESMCEIKDI
IRDQQYNVQLIGTSDKPYVYTDVLA LNSNLCDEKQKVAVEVIKNLLTNTLVLDLLGLGLTLPANKNGIAHLAKSSNFY AQ
LSQQFDAKESEVRVLRVDFANKEVKNCAGVLRPFLQHIAVATLRCLTADTVEKAKSGHPGMPIGMSPIAYVLWKFFFKS
SKDDVNWLNRDRFVLSNGHGCTLLYAMLHLTDCNLSLDDLKNFRSLHSKTPGHPEYGHTEGVDATTGPLGQGV CNAIGMA
LSEAHLAARFNKDGQNI FDHHTYVFLGDGCLMERVAMEGLSFAGHQKLNKLIVFYDDNSITIDGKTELFTQNTPEVMRG
FGWHVIVVDKADNDLVGIKEAILEAHTVTDKPIMIVCKTTIGYSSKVQGTAKVHGSPLGADGLKNLKETCGFTGNDFFHV
PEIVRKDFATVINRNSEKLSQWKQVKSAYDTTHATESQLLQRMINHELEGDVMEKLPKYLEQKKIATRSTSQQVLN AIYP
LIPSLVGGSADLTSPSNLTDVTGCQDFQPNNRVGRYIRFGVREHAMVAIANGILYHGVLRTYVGTFLNFASYALGAIRLSA
LSGLPNIYVFTHDSIGLGQDGP THQPVEVLPMLIAIPNHIVFRPADGRETS GAYLWAVQSKKTPSSMILSRQDLPQLTGT
DISKVALGAYVIQGDATPDVVLVGTGSEVSLMVEAAEKLKANLKNVVSMPSWELFVRQSE EYRKTVFPDGI PVVSAEAS
STFGWTSFAHYAVGMTTFGASAAAEEVYKLLKITS DNVAEKATKLVTKYKGQAPRLSLSLVGEEL

005260-005260

Figure 6. The DNA sequence of the 1068 bp *Naegleria* thiaminase I segment, as cloned in pNB1+ and expressed from the 3414 base genomic sequence of gene TTK.

ATGTCCACTCAACCAAGACACTCACTGTTGGTCTCTCCCATATCTTCCTTCTTGAATGAAAATGGCAACGAAGTTAA
ATTGATCAATTTGATCAAGGATGTTTTGCCAACTCAGGTTTCCGGATATAATATCGAATATACCGAATTTGATTGTTACA
GTGATGCTAGTCTTCAAAGTCTTCCAGATGTTTTCTCAACTGATAGCATTTTCCTTCCATATCTTGTTTCTTTGGGTGGT
GTCAAGAGTTTGGATGAATCATTGGTTCGTGGTGTACTGGTGATTTGCATAGTTTGTTCCTCAAGTGCCTCTGTCAA
TGGTTCCGTTTATGGTTTCCCACTACTTGTGCTCAAACCTTTTATTGTCTCACCAAATGGTACTCAACAAGCATCTT
CCCTTTTAGAATTGGCTCAAAAGGTTGGTTATGAACAAATGTTTATCCAGATGTTGCCTCTTCTAGTCTTTTACAGTT
TTCGGATTGTATCAACAATTACTCCAATCATCATCATCAGCTGCAGTTGATATCAAGGCCTCTGATCTTCCACAATCTGG
TGACCAAGTCAACAAGGATATCACTCAAAAATATAGAACCATTGTTGGATTCAACAGTTGTTGCCTCTCAAAGAGAATATA
TTAACTCTGTAAAGCAAGGTAAACCAATTTCAAACACTACTATGTCGGATATAGTGAAAGTATGTGTGAAATTAAGGATATC
ATCAGAGATCAACAATACAATGTTCAACTCATTTGGTACCTCTGATAAGCCATACGTTTATACTGATGTTTGGCTTTGAA
TTCCAATTTGTGTGATGAAAAGCAAAGGTTGCTGTTGAAGTTATCAAGAATTTATTGACTAATACTTTAGTTTGGACT
TGTTGGGTCTCGGATTAACTCTCCAGCCAACAAGAATGGTATTGCTCATTGGCTAAATCATCAAACCTTTTATGCTCAA
TTGAGCCAACAATTCGATGCCAAGGAAAGTGAAGTTAGAGTTTGTAGATGTGTTGACTTTGCTAACAAGGAAGTTAAGAA
TTGTGCTGGTGTCTTGAGACCATTTCCTT

006260-60552560

Figure 7. The encoded amino acid sequence of the expressed *Naegleria* thiaminase I gene, along with its codons, and with residues numbered (nucleotide/amino acid).

1/1 31/11
ATG TCC ACT CAA CCA AAG ACA CTC ACT GTT GGT CTC TTC CCA TAT CTT CCT TCT TGG AAT
Met ser thr gln pro lys thr leu thr val gly leu phe pro tyr leu pro ser trp asn

61/21 91/31
GAA AAT GGC AAC GAA GTT AAA TTG ATC AAT TTG ATC AAG GAT GTT TTG CCA ACT CAG GTT
glu asn gly asn glu val lys leu ile asn leu ile lys asp val leu pro thr gln val

121/41 151/51
TCC GGA TAT AAT ATC GAA TAT ACC GAA TTT GAT TGT TAC AGT GAT GCT AGT CTT CAA AGT
ser gly tyr asn ile glu tyr thr glu phe asp cys tyr ser asp ala ser leu gln ser

181/61 211/71
CTT CCA GAT GTT TTC TCA ACT GAT AGC ATT TTC CTT CCA TAT CTT GTT TCT TTG GGT GGT
leu pro asp val phe ser thr asp ser ile phe leu pro tyr leu val ser leu gly gly

241/81 271/91
GTC AAG AGT TTG GAT GAA TCA TTG GTT CGT GGT GTT ACT GGT GAT TTG CAT AGT TTT GTT
val lys ser leu asp glu ser leu val arg gly val thr gly asp leu his ser phe val

301/101 331/111
TCC TCA AGT GCC TCT GTC AAT GGT TCC GTT TAT GGT TTC CCA CAA TAC TTG TGC TCA AAC
ser ser ser ala ser val asn gly ser val tyr gly phe pro gln tyr leu cys ser asn

361/121 391/131
TTT TTA TTG TCC TCA CCA AAT GGT ACT CAA CAA GCA TCT TCC CTT TTA GAA TTG GCT CAA
phe leu leu ser ser pro asn gly thr gln gln ala ser ser leu leu glu leu ala gln

421/141 451/151
AAG GTT GGT TAT GAA CAA ATT GTT TAT CCA GAT GTT GCC TCT TCT AGT TCT TTC ACA GTT
lys val gly tyr glu gln ile val tyr pro asp val ala ser ser ser ser phe thr val

481/161 511/171
TTC GGA TTG TAT CAA CAA TTA CTC CAA TCA TCA TCA TCA GCT GCA GTT GAT ATC AAG GCC
phe gly leu tyr gln gln leu leu gln ser ser ser ser ala ala val asp ile lys ala

541/181 571/191
TCT GAT CTT CCA CAA TCT GGT GAC CAA GTC AAC AAG GAT ATC ACT CAA AAA TAT AGA ACC
ser asp leu pro gln ser gly asp gln val asn lys asp ile thr gln lys tyr arg thr

601/201 631/211
ATT TTG GAT TCA ACA GTT GTT GCC TCT CAA AGA GAA TAT ATT AAC TCT GTA AAG CAA GGT
ile leu asp ser thr val val ala ser gln arg glu tyr ile asn ser val lys gln gly

661/221 691/231
AAA CCA ATT TCA AAC TAC TAT GTC GGA TAT AGT GAA AGT ATG TGT GAA ATT AAG GAT ATC
lys pro ile ser asn tyr tyr val gly tyr ser glu ser met cys glu ile lys asp ile

721/241 751/251
ATC AGA GAT CAA CAA TAC AAT GTT CAA CTC ATT GGT ACC TCT GAT AAG CCA TAC GTT TAT
ile arg asp gln gln tyr asn val gln leu ile gly thr ser asp lys pro tyr val tyr

781/261 811/271
ACT GAT GTT TTG GCT TTG AAT TCC AAT TTG TGT GAT GAA AAG CAA AAG GTT GCT GTT GAA
thr asp val leu ala leu asn ser asn leu cys asp glu lys gln lys val ala val glu

841/281 871/291
GTT ATC AAG AAT TTA TTG ACT AAT ACT TTA GTT TTG GAC TTG TTG GGT CTC GGA TTA ACT
val ile lys asn leu leu thr asn thr leu val leu asp leu leu gly leu gly leu thr 1

901/301 931/311
CTC CCA GCC AAC AAG AAT GGT ATT GCT CAT TTG GCT AAA TCA TCA AAC TTT TAT GCT CAA
leu pro ala asn lys asn gly ile ala his leu ala lys ser ser asn phe tyr ala gln

961/321 991/331
TTG AGC CAA CAA TTC GAT GCC AAG GAA AGT GAA GTT AGA GTT TTG AGA TGT GTT GAC TTT
leu ser gln gln phe asp ala lys glu ser glu val arg val leu arg cys val asp phe

1021/341 1051/351
GCT AAC AAG GAA GTT AAG AAT TGT GCT GGT GTC TTG AGA CCA TTC CTT
ala asn lys glu val lys asn cys ala gly val leu arg pro phe leu

00000-0052500

Figure 8. Comparison of the amino acid sequence of *Naegleria* thiaminase 1 (N40KAT) aligned with the sequences of *Bacillus* thiaminase (BSTP) and segments of the transketolases of six organisms. The numbering system indicated here is for the yeast transketolase.

Abbrev.	Genbank	Enzyme and Organism
ScTKT1ct	- P23254	Transketolase of <i>Saccharomyces cerevisiae</i>
CpTKT7ct	- Q42677	Transketolase of <i>Craterostigma plantagineum</i>
EcTKT2ct	- P33570	Transketolase of <i>Escherichia coli</i>
BsTKTct	- P45694	Transketolase of <i>Bacillus subtilis</i>
MgTKT	- P47312	Transketolase of <i>Mycoplasma genitalium</i>
MjPTK1	- Q58092	Transketolase of <i>Methanococcus jannaschii</i>
BSTP	- P45741	Thiaminase I precursor from <i>Bacillus thiaminolyticus</i>
N40KAT	- ---->	Thiaminase I of <i>Naegleria gruberi</i> , aa 1-356

ScTKT1ct	ADDVK---QLKSKFGFNPDKSFVVPQEVYD-HYQKTLKPGVEANNKWNKLFSEYQKKFP	56
CpTKT7ct	PKEAE---ATRKNLGW-PYEPFHVPDDVKK-HWSRHIAE-GAALESAWNNAKFAEFQKKFP	
EcTKT2ct	EEEVA---LARQKLGW-HHPFFEIPKEYI--HAWDAREK-GEKAQQSWNEKFAAYKKAHP	
BsTKTct	KEESK---LTKEAYAWTYEEDFYVPSEVYE-HFAVAVKESGEKKEQEWNAQFAKYKEVYP	
MgTKT	EVDFQ---LFEKRTNT-NFNFFNYPDSIYH-WFKQTVIERQKQIKEDYNLLISLKD-K-P	
MjPTK1	-----	
BsTP	MSKVKGFIYKPLMVMLALLLVVSPAGAGAAHSDASSDITLKVAIYPYVDPARFQAAVL	
N40KAT	MSTQP----KTLTVGLFPYL----PS-----WNENGNEVKLINLIKDVLP-----	

ScTKT1ct	ELGAELARRLSGQLPANWESKLPTYTAKDSA----VATRKLSSETVLEDVYNQLPELIGGS	112
CpTKT7ct	EEAADLKSIIITGELPTNWESIFPTYTPENPG----LPTRTLSHQILNGLGDVLPGLLGGS	
EcTKT2ct	QLAEETFTRMSGGLPKDWEKTTQKYINELQANPAKIATRKAQNTLNAYGPMPELLGGS	
BsTKTct	ELAEQLELAIKGELPKDWDQEVVPEY-KGSS----LASRASSGEVLNGLAKKIPIFFVGGGS	
MgTKT	-LFKKFTNWIDSDFQALYLNQLDEKKVAKKD----SATRNYLKDFLNQINNPNNSNLYCLN	
MjPTK1	-----MVKLSGVYKG-----MRKGYGETLIELGKKYENLVVLD	
BsTP	DQWQRQEPGVKLEF-TDWDYSADPPDDLVDV----FVLDSIFLSHFVDAGYLLP-FGSQD	
N40KAT	-----QVSGYNIEY-TEFDCYSDASLQSLPD---VFSTDSIFLPYLVSLGGVKSLESLV	

ScTKT1ct	ADLTSPNLTWRKEALDFQPPSSSGSNYSGRYIRYGIREHAMGA---IMNGISAFGANYPYGG	172
CpTKT7ct	ADLTLSNMAFLKNSGDFQKKSPGE-----RNVKFGAREHAMGS---ICNGLALHSPGLLPYCA	
EcTKT2ct	ADLAPSNLTIWKGSVSLKEDPAGN-----YIHVGREFGTA---IANGIAHHG-GFVPYTA	
BsTKTct	ADLAGSNKTTIKNAGDFTAVDYSG-----KNFWFGVREFAMGA---ALNGMALHG-GLRVFVG	
MgTKT	ADVSRS--CFIKIGDDNLHENPCS-----RNIQIGIREFAMAT---IMNGMALHG-GIKVMGG	
MjPTK1	ADLSGS-----TQTAMFAKEFPE-----RFFNAGVAEQNMIG---MAAGLATTG--KIVFAS	
BsTP	IDQAEDVLPFALQGAQRNGEVYGLP-----QILCTNLLFYRKGDCLKIGQVDNIYELYKKIG	
N40KAT	RGVTGDLHSFVSSASVNGSVYGFP-----QYLCSNFFLLSS-----PNGTQQAS-SLLELAQ	

Catalytic Cys

ScTKT1ct	TFLNFVS-YAAGAVR-LSALSGHPVIWVATHDSIGV-GE---DG-PTHQPIET--LAHF	222
CpTKT7ct	TYFVFTD-YMRAAMR-ISALSKARVLYIMTHDSIGL-GE---DG-PTHQPVH--LASF	
EcTKT2ct	TFLMFVE-YARNAAR-MAALMKARQIMVYTHDSIGL-GE---DG-PTHQAVEQ--LASL	
BsTKTct	TFFVFS-D-YLRPAIR-LAALMGLPVTVYVTHDSIAV-GE---DG-PTHEPVEQ--LASL	
MgTKT	TFLAFAD-YSKPAIR-LGALMNLVPVYVYTHDSYQV-GG---DG-PTHQPYDQ--LPML	
MjPTK1	SFSMFASGRAWEIIRNLVAYPKLNVKIVATHAGITV-GE---DG-ASHQMCED--IAIM	
BsTP	TSHSEQIPPPQNKGLLINMAGGTTKASMYLEALIDVTGQYTEYDLLPLDPLNDKVIRGL	
N40KAT	KVGYEQIVYPDVASSSSFTVFGLYQQLQSSSSAAV-----DIKASDLPQSGD-QVNK	

Peptide A -> ASDLPQSGD-QVNK

000000-0052560

Figure 8, continued.

ScTKT1ct	RSLPNIQVWRPADGN-EVSAAYKNSLESKHTPSIIALSRQNLQPQLEGS---SIESASKGG	278
CpTKT7ct	RAMPNILTLPADGN-ETAGAYRAAVQNGERPSILVLAQKLPQLPGT---SIEGVSKGG	
EcTKT2ct	RLTPNFSTWRPCDQV-EAAVGVKLAVERHNGPTALILSRQNLQVVERTPD-QVKEIARGG	
BsTKTct	RAMPNLSLIRPADGN-ETAAAWKLAVQSTDHPTALVLTRQNLPTIDQTSEEALAGVEKGA	
MgTKT	RAIENVCFRPCDEK-ETCAGFNYGLLSQDQTTVLVLRQPLKSIDNTD--SLKTL-KGG	
MjPTK1	RAIPNMVVIAPTDYY-HTKNVIRTIAEYKG-PVYVRMPRRDTEIYENEEATFEIGKKG	
BsTP	RLLINMAGEKPSQYVPEDGDAYVRASWFAQ-GSGRAFIGYSESMRMG---DYAEQVRFK	
N40KAT	DITQKYRTILDSTVV-ASQREYINSVKQKG-PISNYVGYSESMCEIK---DIIRDQQYN	

Peptide B -> TILDSTVV-ASQR

ScTKT1ct	YVLQDVAN-----PDIILVATGSEVSLSVEAAKTLAAKNIKARVVSLPDDFFTFDKQPLE-	332
CpTKT7ct	YVISDNRRGGNSKPDVILIGTGSELEIAARAGDELKKEGKVRVSVLCWELFAEQSEK-	
EcTKT2ct	YVLKDSGG-----KPDIIILATGSEMEITLQAAEKLAGEGRNVRVSVLPSTDIFDAQDEE-	
BsTKTct	YVVSLSKN--E-TPDALLIASGSEVGLAIEAQELAKENIDVSVVSMPSMDRFQKQSD-	
MgTKT	YILLDRKQ-----PDLIIAASGSEVQLAIEFEKVLTKQNVKVRILSVPNITLLKQDEK-	
MjPTK1	ILVDG-----EDLTIIATGEEVPEALRAGEILKENGISAEIVEMATIKPIDEEIHK	
BsTP	PISSSAG-----QDIPLFYSDVSVNSKTAHPELAKLANVMASADTVEQALRPQADGQ	
N40KAT	VQLIGTS-----DKPYVYTDVLAALNSN---LCDEKQKVAVEVIKLLTNTLVLDLLG-	

ScTKT1ct	YRLSVLPDNPVI-MSVEVLATTCWGKYAH-----QSFGIDRFGASGKAPEVFKFFGFTP	385
CpTKT7ct	YRETVLPSGVTARVSVEAGSTFGWERFIGP-KG--KAVGIDRFGASAPAERLFKEFGITV	
EcTKT2ct	YRESVLPNSVAARVAVEAGIADYWKYVGL-KG--AIVGMTGYGESAPADKLPFFFGFTA	
BsTKTct	YKNEVLPAADVKKRLAIEMGSSFGWGKYTGL-EG--DVLGIDRFGASAPGETIINEYGFV	
MgTKT	YLKSLFDANSSL-ITIEASSSYEWFCFKY-VKNHAHLGAFSFGESDDGDKVYQQKGFNL	
MjPTK1	SKDFVVTVEDHSIIGGLGGAVAIEVIAENGLNKKLLRIGINDVFRSGKADELLKYYGLDG	
BsTP	YPQYLLPARHQV-YEALMQDYPIYSELAQIVNK--PSNRVFRLGPEVRT-WLKDAKQVLP	
N40KAT	-LGLTLPAKNG-IAHLAKSSNFYAQLSQ-----QFDAKESEVRVLRVDFANKEV	

Peptide C -> SSNFYAQLSQ-----QFDAK

ScTKT1ct	EGVAERAQKTIAFYKGDKLISPLKKAF	412
CpTKT7ct	EAVVA-AAKEIC-----	
EcTKT2ct	ENIVAKAHKVLGVKGA-----	
BsTKTct	PNVVNRVKALINK-----	
MgTKT	ERIMKIFTSLRN-----	
MjPTK1	ESIAKRIMEEMKKE-----	
BsTP	EALGLTDVSSLAS-----	
N40KAT	KNCAGVLRPFL-----	

000000-000000